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# UniProtKB/Swiss-Prot entry

## P47154

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### Entry information

Entry name	STE24_YEAST
Primary accession number	P47154
Secondary accession numbers	None
Integrated into Swiss-Prot on	February 1, 1996
Sequence was last modified on	February 1, 1996 (Sequence version 1)
Annotations were last modified on	September 2, 2008 (Entry version 73)
Name and origin of the protein	
Protein name	CAAX prenyl protease 1
Synonyms	EC 3.4.24.84
	Prenyl protein-specific endoprotease 1
	PPSEP 1
	A-factor-converting enzyme
Gene name	Name: STE24
	Synonyms: AFC1
	OrderedLocusNames: YJR117W
	ORFNames: J2032
From	Saccharomyces cerevisiae (Baker's yeast) [TaxID: 4932]
Taxonomy	Eukaryota; Fungi; Dikarya; Ascomycota; Saccharomycotina;
	Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
Protein existence	1: Evidence at protein level;

### References

- [1] NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND FUNCTION.  
DOI=10.1083/jcb.136.2.271; PubMed=9015299 [NCBI, ExPASy, EBI, Israel, Japan]  
Fujimura-Kamada K., Nouvet F.J., Michaelis S.;  
"A novel membrane-associated metalloprotease, Ste24p, is required for the first step of NH2-terminal processing of the yeast a-factor precursor."  
J. Cell Biol. 136:271-285(1997).

- [2] NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
STRAIN=ATCC 96604 / S288c / FY1679;  
PubMed=8641269 [NCBI, ExPASy, EBI, Israel, Japan]  
Galibert F., Alexandraki D., Baur A., Boles E., Chalwatzis N., Chuat J.-C., Coster F., Cziepluch C., de Haan M., Domdey H., Durand P., Entian K.-D., Gatiús M., Goffeau A., Grivell L.A., Hennemann A., Herbert C.J., Heumann K., Hilger F., , Karpfinger-Hartl L.;  
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EMBO J. 15:2031-2049(1996).
- [3] FUNCTION.  
DOI=10.1126/science.275.5307.1796; PubMed=9065405 [NCBI, ExPASy, EBI, Israel, Japan]  
Boyartchuk V.L., Ashby M.N., Rine J.;  
"Modulation of Ras and a-factor function by carboxyl-terminal proteolysis.";  
Science 275:1796-1800(1997).
- [4] FUNCTION.  
DOI=10.1083/jcb.142.3.635; PubMed=9700155 [NCBI, ExPASy, EBI, Israel, Japan]  
Tam A., Nouvet F.J., Fujimura-Kamada K., Slunt H., Sisodia S.S., Michaelis S.;  
"Dual roles for Ste24p in yeast a-factor maturation: NH2-terminal proteolysis and COOH-terminal CAA processing.";  
J. Cell Biol. 142:635-649(1998).
- [5] FUNCTION.  
PubMed=9725832 [NCBI, ExPASy, EBI, Israel, Japan]  
Boyartchuk V.L., Rine J.;  
"Roles of prenyl protein proteases in maturation of *Saccharomyces cerevisiae* a-factor.";  
Genetics 150:95-101(1998).
- [6] FUNCTION.  
DOI=10.1074/jbc.275.9.6227; PubMed=10692417 [NCBI, ExPASy, EBI, Israel, Japan]  
Schmidt W.K., Tam A., Michaelis S.;  
"Reconstitution of the Ste24p-dependent N-terminal proteolytic step in yeast a-Factor biogenesis.";  
J. Biol. Chem. 275:6227-6233(2000).
- [7] CHARACTERIZATION.  
DOI=10.1128/MCB.20.12.4381-4392.2000; PubMed=10825201 [NCBI, ExPASy, EBI, Israel, Japan]  
Trueblood C.E., Boyartchuk V.L., Picologlou E.A., Rozema D., Poulter C.D., Rine J.;  
"The CaaX proteases, Afc1p and Rce1p, have overlapping but distinct substrate specificities.";  
Mol. Cell. Biol. 20:4381-4392(2000).
- [8] SUBCELLULAR LOCATION.  
DOI=10.1073/pnas.95.19.11175; PubMed=9736709 [NCBI, ExPASy, EBI, Israel, Japan]  
Schmidt W.K., Tam A., Fujimura-Kamada K., Michaelis S.;  
"Endoplasmic reticulum membrane localization of Rce1p and Ste24p, yeast proteases involved in carboxyl-terminal CAAX protein processing and amino-terminal a-factor cleavage.";  
Proc. Natl. Acad. Sci. U.S.A. 95:11175-11180(1998).
- [9] LEVEL OF PROTEIN EXPRESSION [LARGE SCALE ANALYSIS].  
DOI=10.1038/nature02046; PubMed=14562106 [NCBI, ExPASy, EBI, Israel, Japan]  
Ghaemmaghami S., Huh W.-K., Bower K., Howson R.W., Belle A., Dephoure N., O'Shea E.K., Weissman J.S.;  
"Global analysis of protein expression in yeast.";  
Nature 425:737-741(2003).
- [10] TOPOLOGY [LARGE SCALE ANALYSIS].  
DOI=10.1073/pnas.0604075103; PubMed=16847258 [NCBI, ExPASy, EBI, Israel, Japan]  
Kim H., Melen K., Oesterberg M., von Heijne G.;  
"A global topology map of the *Saccharomyces cerevisiae* membrane proteome.";  
Proc. Natl. Acad. Sci. U.S.A. 103:11142-11147(2006).

Comments

- **FUNCTION:** Proteolytically removes the C-terminal three residues of farnesylated A-factor mating pheromone. Also acts to cleave the N-terminal extension of the pheromone. Does not act on Ras.
- **CATALYTIC ACTIVITY:** The peptide bond hydrolyzed can be designated -C-I-A-A-X in which C is an S-isoprenylated cysteine residue, A is usually aliphatic and X is the C-terminal residue of the substrate protein, and may be any of several amino acids.
- **COFACTOR:** Binds 1 zinc ion per subunit (*By similarity*).
- **INTERACTION:**  
P10592::SSA2; NbExp=1; IntAct=EBI-18298, EBI-8603;
- **SUBCELLULAR LOCATION:** Endoplasmic reticulum membrane; Multi-pass membrane protein.
- **MISCELLANEOUS:** Present with 19600 molecules/cell in log phase SD medium.
- **SIMILARITY:** Belongs to the peptidase M48A family [view classification].

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## Cross-references

## Sequence databases

EMBL U77137; AAB38271.1; -, Genomic\_DNA.[EMBL / GenBank / DDBJ] [CoDingSequence]  
Z49617; CAA89647.1; -, Genomic\_DNA.[EMBL / GenBank / DDBJ] [CoDingSequence]  
PIR S57140; S57140.  
RefSeq NP\_012651.1; -.

## 3D structure databases

ModBase P47154.

## Protein-protein interaction databases

DIP DIP:1390N; -.  
IntAct P47154; -.

## Protein family/group databases

MEROPS M48.001; -.

## Organism-specific databases

CYGD YJR117w; -.  
SGD S000003878; STE24.  
Yeast-GFP YJR117W.

## Gene expression databases

GermOnline YJR117W; *Saccharomyces cerevisiae*.

## Ontologies

GO:0030176; Cellular component: integral to endoplasmic reticulum membrane (*inferred from direct assay from SGD*).  
GO:0005741; Cellular component: mitochondrial outer membrane (*inferred from direct assay from SGD*).  
GO:0008487; Molecular function: prenyl-dependent CAAX protease activity (*inferred from direct assay from SGD*).  
GO:0005515; Molecular function: protein binding (*inferred from physical interaction from IntAct*).  
GO:0007323; Biological process: peptide pheromone maturation (*inferred from direct assay from SGD*).  
QuickGo  
view.

## Family and domain databases

InterPro IPR006025; Pept\_M\_Zn\_BS.  
IPR001915; Peptidase\_M48.  
Graphical view of domain structure.

**Pfam** PF01435; Peptidase\_M48; 1.  
 Pfam graphical view of domain structure.  
**PROSITE** PS00142; ZINC\_PROTEASE; 1.  
**BLOCKS** P47154.  
**Proteomic databases**  
 PeptideAtlas P47154; -.  
**Genome annotation databases**  
 Ensembl YJR117W; *Saccharomyces cerevisiae*. [Contig view]  
 GeneID 853581; -.  
 GenomeReviews Y13136\_GR; YJR117W.  
 KEGG sce:YJR117W; -.  
 NMPDR fig|4932.3.peg.3626; -.  
**Phylogenomic databases**  
 HOGENOM P47154; -.  
**Other**  
 LinkHub P47154; -.  
 ProtoNet P47154.  
 UniRef View cluster of proteins with at least 50% / 90% / 100% identity.

### Keywords

Complete proteome; Endoplasmic reticulum; Hydrolase; Membrane; Metal-binding; Metalloprotease; Pheromone response; Protease; Transmembrane; Zinc.

### Features



Feature table viewer



Feature aligner

Key	From	To	Length	Description	FTId
CHAIN	1	453	453	CAAX prenyl protease 1.	PRO_0000138846
TOPO_DOM	1	12	12	Lumenal (Potential).	
TRANSMEM	13	33	21	Potential.	
TOPO_DOM	34	89	56	Cytoplasmic (Potential).	
TRANSMEM	90	110	21	Potential.	
TOPO_DOM	111	121	11	Lumenal (Potential).	
TRANSMEM	122	142	21	Potential.	
TOPO_DOM	143	167	25	Cytoplasmic (Potential).	
TRANSMEM	168	188	21	Potential.	
TOPO_DOM	189	197	9	Lumenal (Potential).	
TRANSMEM	198	218	21	Potential.	
TOPO_DOM	219	306	88	Cytoplasmic (Potential).	
TRANSMEM	307	327	21	Potential.	
TOPO_DOM	328	357	30	Lumenal (Potential).	
TRANSMEM	358	378	21	Potential.	
TOPO_DOM	379	453	75	Cytoplasmic (Potential).	
ACT_SITE	298	298		By similarity.	
ACT_SITE	394	394		Proton donor (By similarity).	
METAL	297	297		Zinc; catalytic (By similarity).	
METAL	301	301		Zinc; catalytic (By similarity).	
METAL	390	390		Zinc; catalytic (By similarity).	

### Sequence information

Length: 453 AA [This is the length of the unprocessed precursor]

Molecular weight: 52324 Da [This is the MW of the unprocessed precursor]

CRC64: 331CC9AE2D7C99DA [This is a checksum on the sequence]

10	20	30	40	50	60
MFDLKTILDH	PNIPWKLIIS	GFSIAQFSFE	SYLTYRQYQK	LSETKLPPVL	EDEIDDETFF
70	80	90	100	110	120
KSRNYSRAKA	KFSIFGDVYN	LAQKLVFIKY	DLFPKIWHMA	VSLNNAVLFPV	RFHVMSTVAQ
130	140	150	160	170	180
SLCFLGLLSS	LSTLVDLPLS	YYSHFVLEEK	FGFNKLTVQL	WITDMIKSLT	LAYAIGGPIL
190	200	210	220	230	240
YLFLKIFDKF	PTDFLWYIMV	FLFVVQILAM	TIIPVFIMP	FNKFTPLEDG	ELKKSIESLA
250	260	270	280	290	300
DRVGFLDKI	FVIDGSKRSS	HSNAYFTGLP	FTSKRIVLFD	TLVNSNSTDE	ITAVLAHEIG
310	320	330	340	350	360
HWQKNHIVNM	VIFSQQLHTFL	IFSLFTSIYR	NTSFYNTFGF	FLEKSTGSFV	DPVITKEFPI
370	380	390	400	410	420
IIGFMLFNDL	LTPLECAMQF	VMSLISRTHE	YQADAYAKKL	GYKQNLCLAL	IDLQIKNLST
430	440	450			
MNVDPYSSY	HYSHPTLAER	LTALDYPVSEK	KKN		

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BLAST

BLAST submission on  
ExPASy/SIB  
or at NCBI (USA)



Sequence analysis tools: ProtParam, ProtScale,  
Compute pI/Mw, PeptideMass, PeptideCutter,  
Dotlet (Java)



ScanProsite, MotifScan



Submit a homology modeling request to SWISS-MODEL



NPSA Sequence analysis  
tools




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